

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BLACK, ROY A
SLEATH, PAUL R
KRONHEIM, SHIRLEY R

(ii) TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN 1B PROTEASE INHIBITORS

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER & MILNAMOW
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(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: KATZ, MARTIN L.
(B) REGISTRATION NUMBER: 25011
(C) REFERENCE/DOCKET NUMBER: IMMUNEX2108

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAAGGAGAG AAAAGCCTAA AAGAGAGTGG GTAGATGGCC GACAAGGTCC TGAAGGAGAA	60
GAGAAAGCTG TTTATCCGTT CCATGGGTGA AGGTACAATA AATGGCTTAA GGTAGAAGGT	120
GAAGGAAATA CTGGATGAAT TATTACAGAC AAGGGTGCTG AACAAAGGAAG AGATGGAGAA	180
AGTAAAACGT GAAAATGCTA CAGTTTATAG AAAAGAAGAA CGCTTATGGA TAAGACCCGA	240
GCTTGATTG ACTCCGTTAT TCCGAAAGGG GCACAGGCAT GCCAAATTG CATCACATAC	300
CGGATAAGTG AAAGTGATAA TTTGTGAAGA AGACAGTTAC CTGGCAGGGA CGCTGGGACT	360
CTCAGCAGAT CAAACATCTG GAAATTACCT TAATTGAGGA AAGAAAGAAA ATTATGCAAG	420
ACTCTCAAGG AGTACTTTCT TCCTTCAG CTCCTCAGGC AGTGCAGGAC AACCCAGCTA	480
TGCCACAGG GAACGGAAGA GTGAATCCTC AGGCTCAGAA GGGAAATGTCA AGCTTGCTC	540
CCTAGAAGAA GCTCAAAGGA TATGGAAACA AAAGTCGGCA GTTAAGTAGA ACAGGAGAGA	600
TTTATCCAAT AATGGACAAG TCAAGCCGCA CACGTCTTGC TCTCATTATC TGCAATGAAG	660
AATTGACAG TAGAGTGAAG AATGTTGAG TAATTCTAG AAGAACTGGA GCTGAGGTTG	720
ACATCACAGG CATGACAATG CTGCTACAAA ATCTGGGTA CAGCGTAAAA TAAATTGGA	780
AAAAGGGATG TGAAAAAAA TCTCACTGCT TCGGACATGA CTACAGAGCT GGAGGCATTT	840
GCACACCGCC CAGAGCACAA GTATATGAGG GCGGACCTCT GACAGCACGT TCCTGGTGT	900
CATGTCTCAT GGTATTCGGG AAGGCATTG TGGGAAGAAA CACTCTGAGG AAGAAAATAT	960
ACACAAGTCC CAGATATACT ACAACTCAAT GCAATCTTA ACATGTTGAA TACCAAGAAC	1020
TGCCCAAGTT TGAAGGACAG AACAGGAGAA TAAGAAACCG AAGGTGATCA TCATCCAGGC	1080
CTGCCGTGGT GACAGCCCTG GTGTGGTGTG GTTAAAGAT TCAGTAGGAA GATTGGAAA	1140
AAAGGTTCT GGAAACCTAT CTTTACCAAC TACAGAAGAG TTTGAGGATG ATGCTATTAA	1200
GAAAGCCCAC ATAGAGAAGA AACTAAATAG TTGAGATTT ATCGCTTCT GCTCTCCAC	1260
ACCAGATAAT GTTCTTGGA GACATCCCAC AATGGGCTCT GTTTTATTG AGGTGGTAAC	1320
CAAGGAGAAG GGAAGACTCA TTGAACATAT GCAAGAATAT GCCTGTTCT GTGATGTGGA	1380
GGAAATTTTC CGCAAGGTTC GATTTGGAGA GAAGTTGAG ATTAGCTCA TTTGAGCAGC	1440
CAGATGGTAG AGCGCAGATG CCCACCACTG AAAGAGTGAC TTTGACAAGA TGTTCTACC	1500

TCGTTCCAG GACATTAAAA TAAGGAAACT GTATGAATGT CTGCGGCAG GAAGTGAAGA 1560
GATCGTTCTG TAAAAGGTTT TTGGAATTAT GTCTGCTGAA TAATAAACTT TTTTGAAAT 1620
AATAAAATCTG GTAGAAAAAT GAAAAAAA AAAAAAAA 1659

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

M t Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
1 5 10 15
Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
20 25 30
Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
35 40 45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
50 55 60
Gly Ala Gln Ala Cys Gln Ile Cyc Ile Thr Tyr Ile Cys Glu Glu Asp
65 70 75 80
Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
85 90 95
Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
100 105 110
Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
115 120 125
Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile
130 135 140
Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
145 150 155 160
Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
165 170 175

Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
180 185 190

Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
195 200 205

Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
210 215 220

Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
225 230 235 240

Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
245 250 255

Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
260 265 270

Leu Lys Asp Lys Pro Lys Val Ile Ile Gln Ala Cys Arg Gly Asp
275 280 285

Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
290 295 300

Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
305 310 315 320

Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
325 330 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
340 345 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu
355 360 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
370 375 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu
385 390 395 400

Phe Pro Gly His

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ala Glu Val Pro Glu Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser
1 5 10 15

Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met
20 25 30

Lys Cys Ser Phe GIn Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile
35. 40 45

GIn Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala
50 55 60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro
65 70 75 80

Cys Pro GIn Thr Phe GIn Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe
85 90 95

Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala
100 105 110

Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp
115 120 125

Ser GIn GIn Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala
130 135 140

Leu His Leu GIn Gly GIn Asp Met Glu GIn GIn Val Val Phe Ser Met
145 150 155 160

Ser Phe Val GIn Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu
165 170 175

Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp
180 185 190

Lys Pro Thr Leu GIn Leu GIu Ser Val Asp Pro Lys Asn Tyr Pro Lys
195 200 205

Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn
210 215 220

Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr
225 230 235 240

Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly
245 250 255

Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser
260 265

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TACCGGGCTGT TCCAGGAC 18

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TACCTATTCT GGGCTCGA 18

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TTGGTCGATA CGGGTGT 17

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CACCAACACCA AATTCTCA 18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATGGAGAAGG GTCCTGTA 18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTCGAATTCA AYCCNGCNAT GCCNAC 26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTCTCTAGAA GYTTNACRTT NCCYTC 26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATATCGGTAC CGCCTCCAGC ATGCCCTCCGG CAATGCCAC ATC 43

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTGCTAGATC TGCCCGCAGA CATTCACTACA G 31

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Tyr Val His Asp Ala Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ala Tyr Val His Asn Ala Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ala Tyr Val His Glu Ala Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (B) LOCATION: 4
 - (C) IDENTIFICATION METHOD: Xaa = D-Asp
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Ala Tyr Val His Xaa Ala Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala Tyr Val His Asp Gly Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ala Tyr Val His Asp Val Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ala Tyr Val Phe Asp Ala Pro Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Ala Tyr Val His Asp Ala Ala Val Arg Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Glu Ala Tyr Val His Asp Ala Pro Val Arg Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Tyr Val His Asp Ala Pro Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Val His Asp Ala Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

His Asp Ala Pro
1